at the tip of the ''blade'' was operated, we analyzed actin dynamics and the traction force pattern on elastic substrates. The obtained quantitative data will be used to develop a biophysical model of the convergence of cell edge oscillations into a polarized state. This work was supported by an NCCBI interdisciplinary PhD fellowship.

1668-Pos Board B578
Cyto-Mechanics of Microtubular Buckling and Centering of Centrosome
Gaurav Misra, Anthony J.C. Ladd, Tanmay P. Lele, Robert Russel, Jun Wu, Richard B. Dickinson.
Despite being fundamental to the understanding of several cellular processes, cytoskeletal mechanics is poorly understood primarily due to the multi-scale physical and chemical complexity of cells. Positioning of the centrosome is central to cytoskeletal organization and basic processes like migration and division. In patterned cells, the centrosome localizes at the geometric center of the pattern through an unknown mechanism. While it is known that the microtubules (MTs) growing out from the centrosome mediate the forces acting on it, whether the forces on the centrosome are compressive or tensile is not established. On one hand, MTs impinging against the cell membrane are thought to center the centrosome through pushing forces. On the other hand, cortex-bound dynein motors are implicated to render centering through pulling forces on the MTs. As theoretical support for the latter mechanism, we have developed a computational model for the dynamics of the microtubular aster coupled with a model for the dynein motors, which are assumed to be tethered to the cortex at the light-chain end and pulling on the MTs at the heavy-chain end. The MTs are modeled as elastic filaments growing stochastically from the centrosome and exhibiting dynamic instability. Buckling of MTs in a cell is widely considered as an evidence for existence of compressive forces along the entire length of the MTs, thereby invoking the pushing mechanism for centrosome centering. However, we demonstrate that even buckled MTs can be under tension along most of their length and hence can transmit the pulling forces of the dynein motors to the centrosome. Simulations show that dynein-generated tensile forces on centrosome-anchored MTs naturally lead to centering of centrosome. The predicted relaxation time in positional fluctuations of centrosome agrees quantitatively with the measured value obtained by tracking centrosome in live cells.

Photosynthesis & Photoreceptors

1669-Pos Board B579
Thermal Properties of Rhodopsin: Insight into Molecular Mechanism of Dim-Light Vision
Jian Liu, Monica Liu, Jennifer Nguyen, Aditi Bhagat, Victoria Mooney, Elsa C.Y. Yan.
Rhodopsin is one of the best biological light detectors. It detects not only light spanning 6-order magnitude of intensity, but also single photons. Here, we investigated the molecular mechanism for the extremely high quantum yield and low dark noise, which are essential for rhodopsin to gain photosensitivity and function as dim-light photoreceptor. We hypothesize that an extensive intramolecular hydrogen-bonding network increases thermal stability to inhibit thermal isomerization of its 11-cis retinal chromophore, which is the origin of dark noise. We previously found that the rate-determining step of thermal isomerization involves breaking hydrogen bonds. Here, we further tested the hypothesis by perturbing the H-bonding network at the retinal-binding site using two mutations: E181Q and S186A. We expressed and purified the mutants and measured their rates of thermal decay, thermal isomerization, and hydrolysis of the Schiff base. We found that all the rates become 1-2 orders of magnitude faster in the mutants than in wild type. Moreover, we studied the rate of thermal isomerization of 11-cis retinal in solution catalyzed by the wild-type (WT) and mutant opsins. We found that the rate increases by ~20 times in the presence of WT opsin, confirming that opsin can catalyze retinal isomerization in solution. We also found that the rate of the catalytic isomerization remains roughly the same when the WT opsin is replaced by the E181Q and S186A mutant opsins. We conclude that an intact hydrogen-bonding network is essential to stabilize the dark-state rhodopsin to prevent thermal isomerization to achieve low dark-noise. We speculate that the catalytic property of opsin protein is due to optimization of the steric interactions at the active site to pre-determine the trajectory of photo-induced isomerization and increase the quantum yield for light detection in rhodopsin.

1670-Pos Board B580
Intrinsic Photoreception and Photokinesis in T Lymphocytes
Gerard P. Ahern, Sandeep Pingle, Bidhan Bandyopadhyay, Barbara Jaruga.
In mammals, photoreception is believed to be restricted to the eye, and there is little evidence for the existence of non-ocular light detectors. Here we describe direct photon sensing in T lymphocytes that are highly abundant in skin. Blue and ultra-violet light selectively activate a Lck kinase-phospholipase C-gamma1 (PLC-gamma1) signaling pathway that triggers both Ca^{2+} mobilization and Ca^{2+} entry in T cells. The half-maximal Ca^{2+} response occurs with ~10^{17} photons cm^{-2} (480 nm) or within 15 minutes of visible light (400-700nm, 10 mW cm^{-2}). Light-signaling requires an intact T-cell receptor apparatus and occurs independently of known mammalian light sensors, cryptochromes and opsins. Further, light triggers the extension of lamellipodia, and stimulates T cell motility and chemotaxis, with low and high fluence respectively stimulating and inhibiting T cell motility. These data provide evidence for photoreception outside the mammalian eye, and reveal a novel signaling mechanism that may influence T cell function in the skin.

1671-Pos Board B581
Subpicosecond Excited State Proton Transfer Preceding Isomerization during the Photorecovery of Photoactive Yellow Protein
Elizabeth C. Carroll, Masato Kumauchi, Wouter D. Hoff, Delmar S. Larsen.
The ultrafast excited-state dynamics underlying the receptor state photorecovery is resolved in the M100A mutant of the photoactive yellow protein (PYP) from Halorhodospira halophila. The M100A PYP mutant, with its distinctly slower photocycle than wt PYP, allows isolation of the pB signaling state for study of the photodynamics of the protonated chromophore cis-p-coumaric acid. Transient absorption signals indicate a subpicosecond excited-state proton-transfer reaction in the pB state that results in chromophore deprotonation prior to the cis-trans isomerization required in the photorecovery dynamics of the pG state. Two terminal photoproducts are observed, a blue-absorbing species presumed to be deprotonated trans-p-coumaric acid and an ultraviolet-absorbing protonated photoproduct. These two photoproducts are hypothesized to originate from an equilibrium of open and closed folded forms of the signaling state, I2 and I2'.

1672-Pos Board B582
Photorespiratory and Respiratory Carbon Isotope Fractionation in Leaves
Dianne Pater, Erik Erhardt, David T. Hanson.
The photorespiratory pathway in plants is initiated with the uptake of O_2 instead of CO_2 by the photosynthetic enzyme Rubisco. This generates a compound in the leaf that must then be recycled through enzymatic reactions distributed over the leaf chloroplasts, peroxisomes, and mitochondria, resulting in a net loss of CO_2. The pathway was thought to be well understood, but recent studies using mutants lacking expression of the genes coding for peroxisomal malate dehydrogenase (PMDH) have suggested that there are additional mechanisms that alter the stoichiometry of photorespiratory CO_2 release to O_2 uptake. Any changes in this stoichiometry will likely cause a change in the isotopic composition of the CO_2 being released since it would involve additional enzymes or carbon sources. The isotopic composition of the CO_2 being released was measured under both photorespiratory and non-photorespiratory conditions, as well as under different isotopic conditions. Measurements were taken using a tunable diode laser spectroscopy system, which allows high frequency *in vivo* gas exchange measurements of different CO_2 isotopologues. Comparing the PIB isotopic signature of wild type Arabidopsis to that of PMDH mutants, may improve our understanding of alternate metabolic pathways in plants. The decarboxylation fractionation seen is significantly higher in PMDH mutant plants relative to wild-type, which can be partially explained by higher rates of photorespiratory decarboxylation seen in previous studies. The photorespiratory fractionation also varied significantly between wild-type and mutant plants.